Figure 1. Nucleotide sequence including the sequence encoding the aortic carboxypeptidase-like protein of the invention.

GCGGGGGGCAGGAAGGGGCGGGGGGCTCGGCGCACTCGGCAGGAAGAGACCGACCCG
CCACCCGCCGTAGCCCGCGCGCCCCTGGCACTCAATCCCCGCCATGTGGGGGCTCCTGC
TCGCCCTGGCCGCCTTCGCGCCGGCCGTCGGCCCGGCTCTGGGGGCGCCCAGGAACTCG
GTGCTGGGCCTCGCGCAGCCCGGGACCACCAAGGTCCCAGGCTCGACCCCGGCCCTGCA
TAGCAGCCCGGCACAGCCGCCGGCGGAGACAGCTAACGGGACCTCAGAACAGCATGTC
CGGATTCGAGTCATCAAGAAGAAAAAGGTCATTATGAAGAAGCGGAAGAAGCTAACTC
TAACTCGCCCCACCCCACTGGTGACTGCCGGGCCCCTTGTGACCCCCACTCCAGCAGGG
ACCCTCGACCCCGCTGAGAAACAAGAAACAGGCTGTCCTCCTTTGGGTCTGGAGTCCCT
GCGAGTTTCAGATAGCCGGCTTGAGGCATCCAGCAGCCAGTCCTTTGGTCTTGGACCAC
ACCGAGGACGGCTCAACATTCAGTCAGGCCTGGAGGACGGCGATCTATATGATGGAGC
CTGGTGTGCTGAGGAGCAGGACGCCGATCCATGGTTTCAGGTGGACGCTGGGCACCCCA
CCCGCTTCTCGGGTGTTATCACACAGGGCAGGAACTCTGTCTGGAGGTATGACTGGGTC
ACATCATACAAGGTCCAGTTCAGCAATGACAGTCGGACCTGGTGGGGAAGTAGGAACC
ACAGCAGTGGGATGGACGCAGTATTTCCTGCCAATTCAGACCCAGAAACTCCAGTGCTG
AACCTCCTGCCGGAGCCCCAGGTGGCCCGCTTCATTCGCCTGCTGCCCCAGACCTGGCT
CCAGGGAGGCGCGCCTTGCCTCCGGGCAGAGATCCTGGCCTGCCCAGTCTCAGACCCCA
ATGACCTATTCCTTGAGGCCCCTGCGTCGGGATCCTCTGACCCTCTAGACTTTCAGCATC
ACAATTACAAGGCCATGAGGAAGCTGATGAAGCAGGTACAAGAGCAATGCCCCAACAT
CACCCGCATCTACAGCATTGGGAAGAGCTACCAGGGCCTGAAGCTGTATGTGATGGAA
ATGTCGGACAAGCCTGGGGAGCATGAGCTGGGGGAGCCTGAGGTGCGCTACGTGGCTG
GCATGCATGGGAACGAGGCCCTGGGGCGGGAGTTGCTTCTGCTCCTGATGCAGTTCCTG
TGCCATGAGTTCCTGCGAGGGAACCCACGGGTGACCCGGCTGCTCTCTGAGATGCGCAT
TCACCTGCTGCCCTCCATGAACCCTGATGGCTATGAGATCGCCTACCACCGGGGTTCAG
AGCTGGTGGGCTGGGCCGAGGGCCGCTGGAACAACCAGAGCATCGATCTTAACCATAA
TTTTGCTGACCTCAACACACCACTGTGGGAAGCACAGGACGATGGGAAGGTGCCCCACA
TCGTCCCCAACCATCACCTGCCATTGCCCACTTACTACACCCTGCCCAATGCCACCGTGG
CTCCTGAAACGCGGGCAGTAATCAAGTGGATGAAGCGGATCCCCTTTGTGCTAAGTGCC
AACCTCCACGGGGGTGAGCTCGTGGTGTCCTACCCATTCGACATGACTCGCACCCCGTG
GGCTGCCCGCGAGCTCACGCCCACACCAGATGATGCTGTGTTTCGCTGGCTCAGCACTG
TCTATGCTGGCAGTAATCTGGCCATGCAGGACACCAGCCGCCGACCCTGCCACAGCCAG
GACTTCTCCGTGCACGGCAACATCATCAACGGGGCTGACTGGCACACGGTCCCCGGGAG
CATGAATGACTTCAGCTACCTACACACCAACTGCTTTGAGGTCACTGTGGAGCTGTCCT
GTGACAAGTTCCCTCACGAGAATGAATTGCCCCAGGAGTGGGAGAACAACAAAGACGC
CCTCCTCACCTACCTGGAGCAGGTGCGCATGGGCATTGCAGGAGTGGTGAGGGACAAG
GACACGGAGCTTGGGATTGCTGACGCTGTCATTGCCGTGGATGGGATTAACCATGACGT
GACCACGGCGTGGGGCGGGGATTATTGGCGTCTGCTGACCCCAGGGGACTACATGGTG
ACTGCCAGTGCCGAGGGCTACCATTCAGTGACACGGAACTGTCGGGTCACCTTTGAAGA
GGGCCCCTTCCCCTGCAATTTCGTGCTCACCAAGACTCCCAAACAGAGGCTGCGCGAGC
TGCTGGCAGCTGGGGCCAAGGTGCCCCCGGACCTTCGCAGGCGCCTGGAGCGGCTAAG
GGGACAGAAGGATTGATACCTGCGGTTTAAGAGCCCTAGGGCAGGCTGGACCTGTCAA
GACGGGAAGGGGAAGAGTAGAGAGGGAGGGACAAA

Figure 2. Protein sequence encoded by the coding sequence shown in Figure 1.

MWGLLLALAAFAPAVGPALGAPRNSVLGLAQPGTTKVPGSTPALHSSPAQPPAETA
NGTSEQHVRIRVIKKKKVIMKKRKKLTLTRPTPLVTAGPLVTPTPAGTLDPAEKQET
GCPPL**GLESLRVSDSRLEASSSQSFGLGPHRGRLNIQSGLEDGDLYDGAWCAEE**
QDADPWFQVDAGHPTRFSGVITQGRNSVWRYDWVTSYKVQFSNDSRTWWGS
RNHSSGMDAVFPANSDPETPVLNLLPEPQVARFIRLLPQTWLQGGAPCLRAEIL
ACPVSDPNDLFLEAPASGSSDPLDF*QHHNYKAMRKLMKQVQEQCPNITRIYSIGKSYQ*
GLKLYVMEMSDKPGEHELGEPEVRYVAGMHGNEALGRELLLLLMQFLCHEFLRGNPRV
TRLLSEMRIHLLPSMNPDGYEIAYHRGSELVGWAEGRWNNQSIDLNHNFADLNTPLW
EAQDDGKVPHIVPNHHLPLPTYYTLPNATVAPETRAVIKWMKRIPFVLSANLHGGE
LVVSYPFDMTRTPWAARELTPTPDDAVFRWLSTVYAGSNLAMQDTSRRPCHSQDF
SVHGNIINGADWHTVPGSMNDFSYLHTNCFEVTVELSCDKFPHENELPQEWENNKD
ALLTYLEQVRMGIAGVVRDKDTELGIADAVIAVDGINHDVTTAWGGDYWRLLTPG
DYMVTASAEGYHSVTRNCRVTFEEGPFPCNFVLTKTPKQRLRELLAAGAKVPPDLR
RRLERLRGQKD

Figure 3. ClustalW alignment of a protein of the invention.

```
Q61281                        ................................................
O88442                        MAP VRT A SLLC GLL ALL TL C PE GNP Q T VL TDDEIEEFLEG FLSEL E TQS P PREDD VE VQP
Q14113                        ................................................
O54860                        ................................................
AL035460_GENSCAN_predicted_pep ................................................

Q61281                        ................................................
O88442                        LPEP TQR P RKS KAGGK QRAD VE VP PE KNKD KEKKG KKD KG P KATKP L EGS TRP TKKP KEK
Q14113                        ................................................
O54860                        ................................................
AL035460_GENSCAN_predicted_pep ................................................

Q61281                        ................................................
O88442                        P PKA TKKP KEKP PKA TKKP KEKP PKA TKKP KEKP P KATKR P S AGKK FS T VAPL ETL DRLL
Q14113                        ................................................
O54860                        ................................................
AL035460_GENSCAN_predicted_pep ................................................

Q61281                        ................................................
O88442                        PSP SNP S AQEL P QKRD TP FPN AWQGQ GEET QVEAKQ P RPE P EEET EMP TLDYND Q I EKED
Q14113                        ................................................
O54860                        ..............................................MARL GTAC
AL035460_GENSCAN_predicted_pep ................................................

Q61281                        ................................................
O88442                        YEDF EY I RRQKQP RP TPSRRRL WP ER EEKTEEP EE KEVE PPLK LLPPDYGD S Y I PN
Q14113                        ................................................
O54860                        PAL ALAL AL VAVAL A GVRAQG AA FEE DYYS QELWRR GRY YGHP E PEPEPEL FSP S HED
AL035460_GENSCAN_predicted_pep ............MWGLLL AL A AFA AVG PAL GAP NS VL GLAQ ......GT TK PGS

Q61281                        ................................................
O88442                        YDDL YY FPH P P QKP DVGQ EVD EE KE EM KK KKEG S S KED TED KWT VEKN KD HK GP RK
Q14113                        ...MD YY FGP P P QKP DAERQ T DEEKE EL KK KKED S S PKE - ETD KWA VEKG KD HKEP RK
O54860                        LRVE QE QQE HQQ GHRTPKK A I KP K KAP KK E VAE PP P GKNS NRKG RR S NL EKAAS
AL035460_GENSCAN_predicted_pep TPA HS S P AQ P AET ANGTS EQHVR IR V KKK V IMKER K - LTL TRPTPLVTAG PL VTP

Q61281                        ...........................................MQAGANEDDYY
O88442                        GEEL EE WAPVEK IK CPP IG E SHR IE DN Q IRAS SML RHGL GAQR GRL NMQAGANEDDYY
Q14113                        GEEL EE WTP TEK VK CPP GM E SHR IE DN Q IRAS SML RHGL GAQR GRL NMQ TGA EDDYY
O54860                        D HG VP VAHED VRE S CPP GL ETL I TDF L HAS TS KRY GL GAHR GRL N QAGI NE ND Y
AL035460_GENSCAN_predicted_pep TPAGTL DP AEKQET G CPP GLE SL RV SDS R EASS S QSF GL GPHR GRLN QSG LEDGDL Y

Q61281                        D GAWC AE D S QTQWI EVDTRR T TRFT GVI TQGRDSS IHDD F VTT F FVGFSNDS Q TWVMYT
O88442                        D GAWC AE D S QTQWI EVDTRR T TRFT GVI TQGRDSS IHDD F VTT F FVGFSNDSQ TWVMYT
Q14113                        D GAWC AE D AR TQWI EVDTRR T TRFT GVI TQGRDSS IHDD F VTT F FVGFSNDSQ TWVMYT
O54860                        D GAWC A GRNDL H QWI ARRL T FT GVI TQGRN S LWLS V SYK V MVSNDS H T WWT VK
AL035460_GENSCAN_predicted_pep D GAWC AE QD ADP F Q DAGHP TR F GVI TQGRNS VWRYD VTS YK QF SNDS R WWGS R

Q61281                        NGYE - - EMTF GNVD KDTP VLS ELPEP VVARFIR IYPLTWN - GSL CMRLEVL GCP V P
O88442                        NGYE - - EMTF GNVD KDTP VLS ELPEP VVARFIR IYPLTWN - GSL CMRLEVL GCP V P
Q14113                        NGYE - - EMTF GNVD KDTP VLS ELPEP VVARFIR IYPLTWN - GSL CMRLEVL GCS VA - P
O54860                        NGS G - - MI FEGN S EK IP VLN ELP VP V IR INP Q S WFDNGS CMR L GCP PD P
AL035460_GENSCAN_predicted_pep NHS S GMD AV P NS DP TP VLNL LPEP Q WARFIR L P QTWL QGGAP C RAE L CP VS DP

Q61281                        VYS YYA QNEVV TTDS LDFRHHS YKDMRQLMK VNE ECPTI TRTYS LGKSSRGLK I YAMEI
O88442                        VYS YYA QNEVV TTDS LDFRHHS YKDMRQLMK VNE ECPTI TRTYS LGKSSRGLK I YAMEI
Q14113                        VYS YYA QNEVV ATDD LDFRHHS YKDMRQLMK VNE ECPTI TRTYS LGKSSRGLK I YAMEI
O54860                        NNY HRR NEMT TTDD LDFHHNY K MRQLMK VNE MCP N I TRIYN GKSHQGLK I YA E I
AL035460_GENSCAN_predicted_pep NDL LEAP AS G S DP LDF QHHNY K AMRK LMK QV QE QCP N I TRIYS GKS YQGLK L YVME

Q61281                        SDNP G HEL GEP EFRYTAGIH GNEVL GREL LLLLMQYLCQEYRDGNP RVRN L VQD TRIHL
O88442                        SDNP G HEL GEP EFRYTAGIH GNEVL GREL LLLLMQYLCQEYRDGNP RVRN L VQD TRIHL
Q14113                        SDNP GEHEL GEP EFRYTAGIH GNEVL GREL LLLLMQYLC EYRDGNP RVRS L VQD TRIHL
O54860                        SD P G EHE GEP EF HY IAGA H GNEVL GREL LLLL H LCQEY SAQN AR VRL VEE TRIHL
AL035460_GENSCAN_predicted_pep SD KP G EHEL GEP EV RY VAG H GNE AL GREL LLLLMQ LCHE LRGNP RVT RL SEMR IHL

Q61281                        VPSLNP D GYEVAAQMGSEFGNWAL GL WTEEGFDI FEDFPDLNSVL W AEE KWVP YR VPN
O88442                        VPSLNP D GYEVAAQMGSEFGNWAL GL WTEEGFDI FEDFPDLNSVL W AEE KWVP YR VPN
Q14113                        VPSLNP D GYEVAAQMGSEFGNWAL GL WTEEGFDI FEDFPDLNSVL W AEE KWVP YR VPN
O54860                        PSLNP D GYE AVEG GSEL GGWS L GRW HDG ID INNNFPDLNS LWEAEDQQNAP RE VPN
AL035460_GENSCAN_predicted_pep PS NP D GYE AVHR GSEL VGWAE GRWNNQS ID NHNF ADLN P LWEAQDDGK VP H I VPN

Q61281                        NNLP I PERYLSPDATVSTEVRA I I S WMEKNP FVL GANLNGGERL VS YPYDMARTP QEQL
O88442                        NNLP I PERYLSPDATVSTEVRA I I S WMEKNP FVL GANLNGGERL VS YPYDMARTP QEQL
Q14113                        NNLP I PERYLSPDATVSTEVRA I I A WMEKNP FVL GANLNGGERL VS YPYDMARTP QEQL
O54860                        HY AI PE W LSEN AT WATE TRA I AWMEK IP FVL G NL GGEL VA VPYDM RE ......
AL035460_GENSCAN_predicted_pep HH P PT Y TL NAT WAPE TRA I IK WMKR IP FVL S ANL GGEL VS YP DMTRTP .....

Q61281                        LA A A AA ARGED DD V SEAQETPDHA I FRWLAIS FASAHL TMTEP YRGGCQAQD YTS GMG
O88442                        LA A A AA ARGED DD V SEAQETPDHA I FRWLAIS FASAHL TMTEP YRGGCQAQD YTS GMG
Q14113                        LA A A AA ARGED DD V SEAQETPDHA I FRWLAIS FASAHL TMTEP YRGGCQAQD YT GMG
O54860                        ...........LWK - - T Q HT P TP DDH FRWLAVS AS TRL MTDARR RV HTED F QKEE
AL035460_GENSCAN_predicted_pep ...........W ARE LTP TP DD A FRWLS TV AGSN L A QDT S RRP HS DD S VHGN
```

Figure 4: ClustalW Alignment of protein sequences (Mouse CPX1 vs AL035460_A).

```
AF077738                        MWGLLLAVTAFAPSVGLCLGAPSASVPGLA-------PGSTLAPHSSVAQP-STKANETS
AL035460_GENSCAN_predicted_pep  MWGLLLALAAFAPAVGPALGAPRNSVLGLAQPGTTKVPGSTPALHSSPAQPPAETANGTS

AF077738                        ERHVRLRVIKKKIVVKKRK--KLRHPGPLGTARPVVPTHPAKTLTLPEKQEPGCPPLGL
AL035460_GENSCAN_predicted_pep  EQHVRIRVIKKKVIMKKRKKLTLTRPTPLVTAGPLVTPTPAGTLDPAEKQETGCPPLGL

AF077738                        ESLRVSDSQLEASSSQSFGLGAHRGRLNIQSGLEDGDLYDGAWCAEQQDTEPWLQVDAKN
AL035460_GENSCAN_predicted_pep  ESLRVSDSRLEASSSQSFGLGPHRGRLNIQSGLEDGDLYDGAWCAEEQDADPWFQVDAGH

AF077738                        PVRFAGIVTQGRNSVWRYDWVTSCKVQFSNDSQTWWKSR-NSIGMDIVFPANSDAETPVL
AL035460_GENSCAN_predicted_pep  PTRFSGVVTQGRNSVWRYDWVTSCKVQFSNDSRTWWGSRNHSSGMDAVFPANSDPETPVL

AF077738                        NLLPEPQVARFIRLLPQTWFQGGVPCLRAEILACPVSDPNDLFPEAHTLGSSNSLDFRHH
AL035460_GENSCAN_predicted_pep  NLLPEPQVARFIRLLPQTWLQGGAPCLRAEILACPVSDPNDLFLEAPASGSSDPLDFQHH

AF077738                        NYKAMRKLMKQVNEQCPNITRIYSIGKSHQGLKLYVMEMSDHPGEHELGEPEVRYVAGMH
AL035460_GENSCAN_predicted_pep  NYKAMRKLMKQVNEQCPNITRIYSIGKSYQGLKLYVMEMSDKPGEHELGEPEVRYVAGMH

AF077738                        GNEALGRELLLLLMQFLCHEFLRGDPRVTRLLETRIHLLPSMNPDGYETAYHRGSELVG
AL035460_GENSCAN_predicted_pep  GNEALGRELLLLLMQFLCHEFLRGNPRVTRLLEMRIHLLPSMNPDGYEIAYHRGSELVG

AF077738                        WAEGRWTHQGIDLNHNFADLNTQLWYAEDDGLVPDTVPNHHLPLPTYYTLPNATVAPETW
AL035460_GENSCAN_predicted_pep  WAEGRWNNQSIDLNHNFADLNTPLWEAQDDGKVPHIVPNHHLPLPTYYTLPNATVAPETR

AF077738                        AVIKWMKRIPFVLSANLHGGELVVSYPFDMTRTPWAARELTPTPDDAVFRWLSTVYAGTN
AL035460_GENSCAN_predicted_pep  AVIKWMKRIPFVLSANLHGGELVVSYPFDMTRTPWAARELTPTPDDAVFRWLSTVYAGSN

AF077738                        RAMQDTDRRPCHSQDFSLHGNIINGADWHTVPGSMNDFSYLHTNCFEVTVELSCDKFPHE
AL035460_GENSCAN_predicted_pep  LAMQDTSRRPCHSQDFSLHGNIINGADWHTVPGSMNDFSYLHTNCFEVTVELSCDKFPHE

AF077738                        KELPQEWENNKDALLTYLEQVRMGITGVVRDKDTELGIADAVIAVEGINHDVTTAWGGDY
AL035460_GENSCAN_predicted_pep  NELPQEWENNKDALLTYLEQVRMGIAGVVRDKDTELGIADAVIAVEGINHDVTTAWGGDY

AF077738                        WRLLTPGDYVVTASAEGYHTVRQHCQVTFEEGPVPCNFLLTKTPKERLRELLATRCKPP
AL035460_GENSCAN_predicted_pep  WRLLTPGDYVVTASAEGYHSVTRNCRVTFEEGPFPCNFVLTKTPKQRLRELLAAGAKPP

AF077738                        DLRRKLERLRGQK-
AL035460_GENSCAN_predicted_pep  DLRRKLERLRGQKD
```
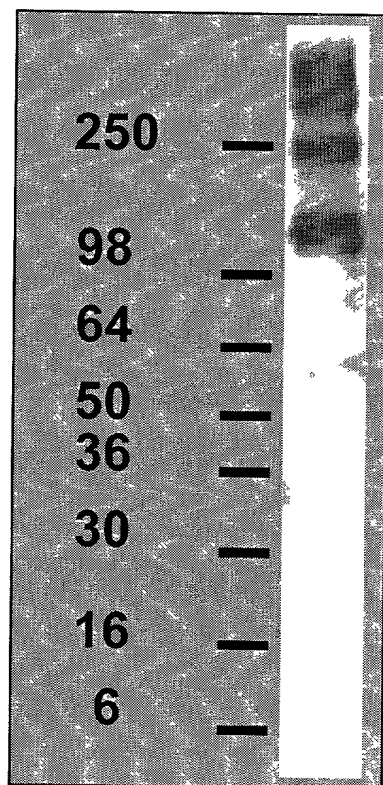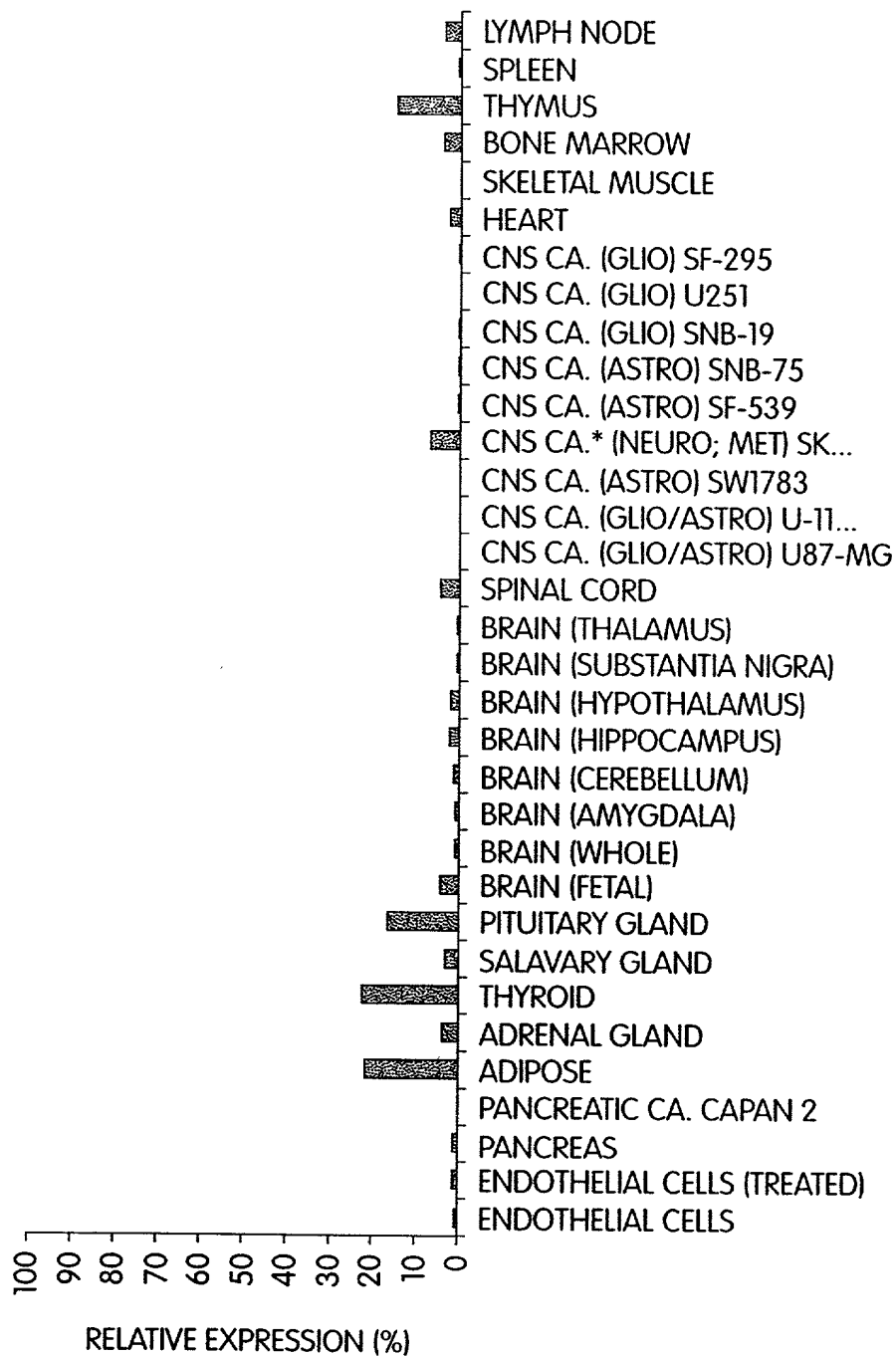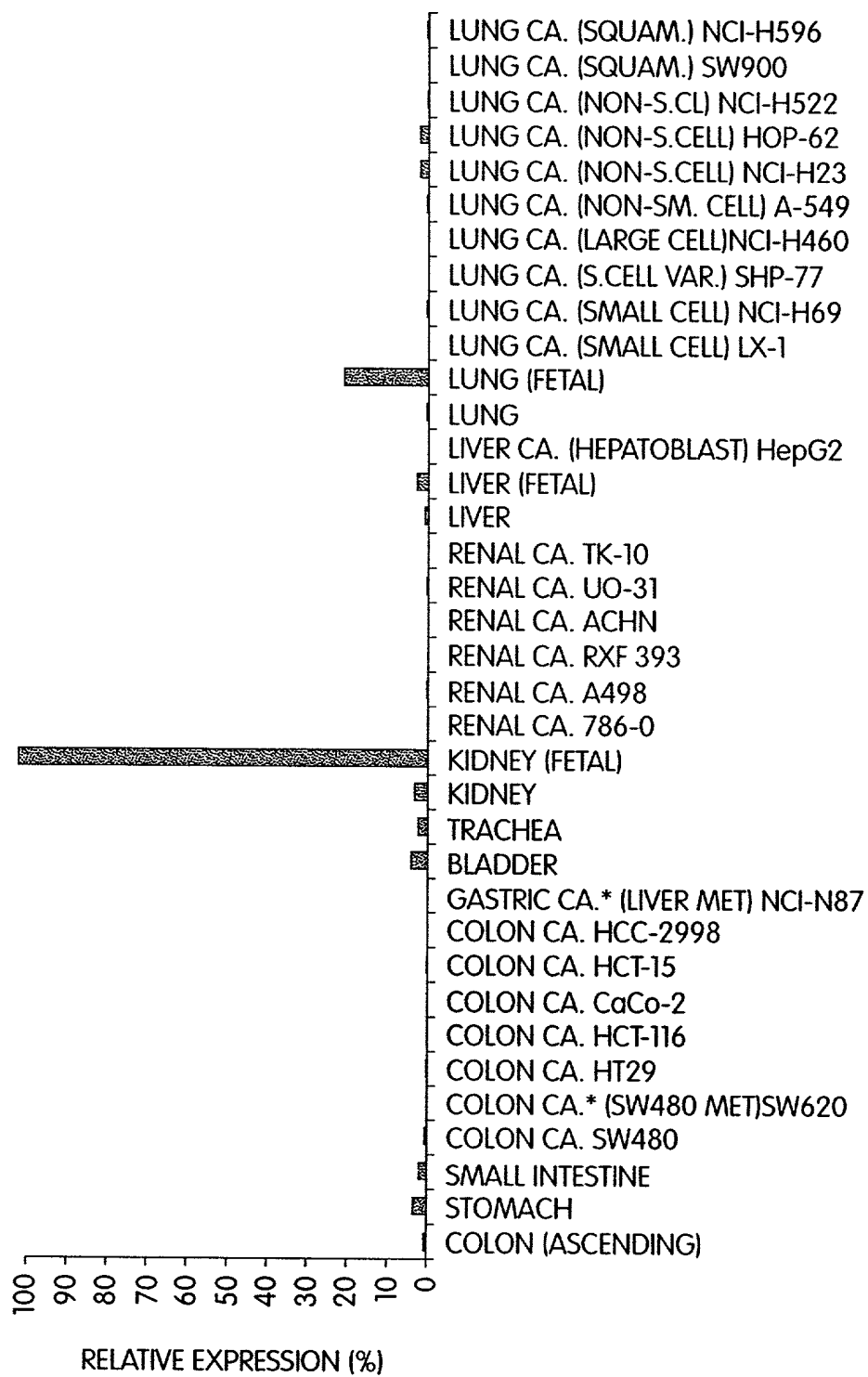
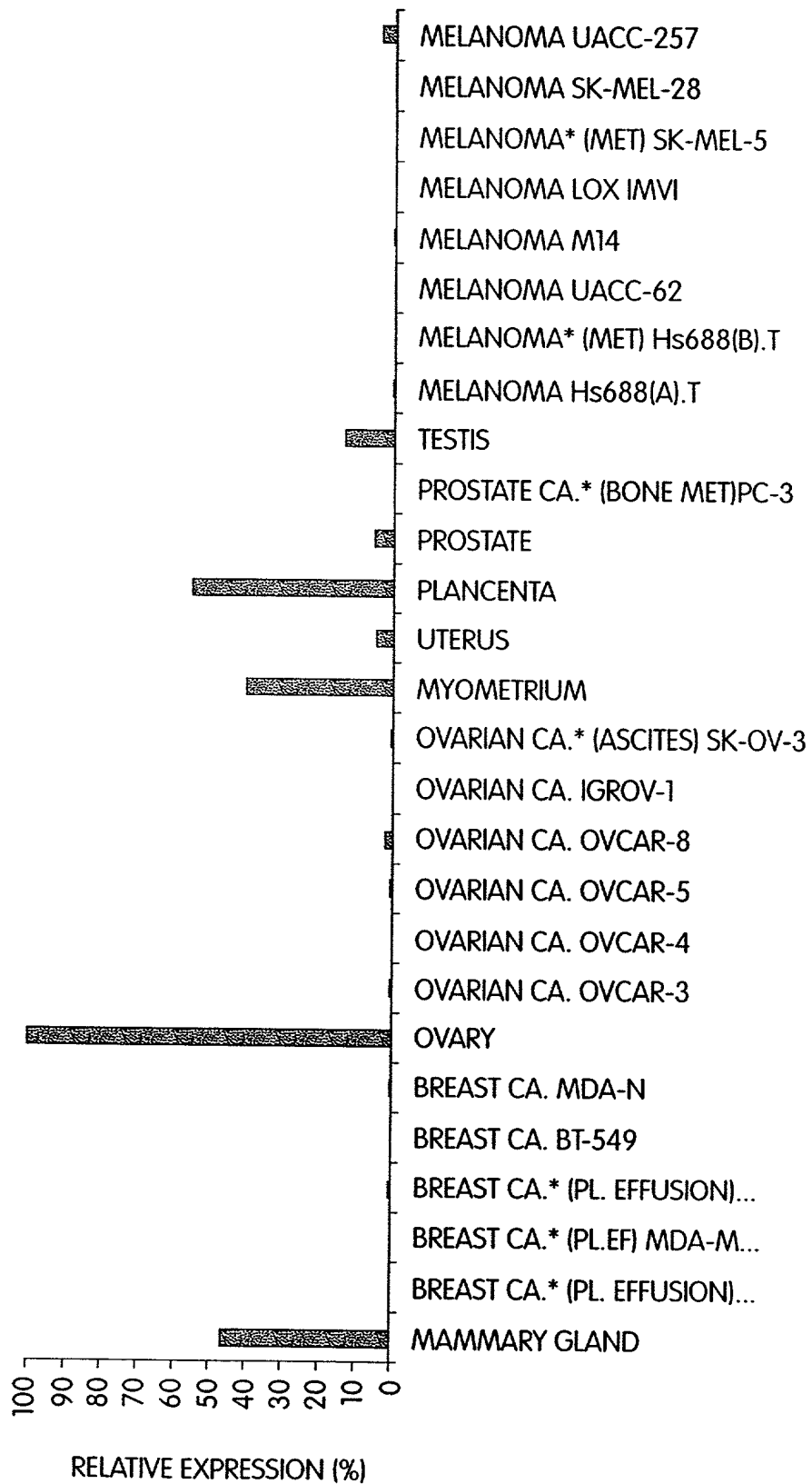**Figure 5. Western blot SDS-PAGE of hAL035460A protein secreted by 293 cells.**

Fig. 6A

Fig. 6B

RELATIVE EXPRESSION (%)
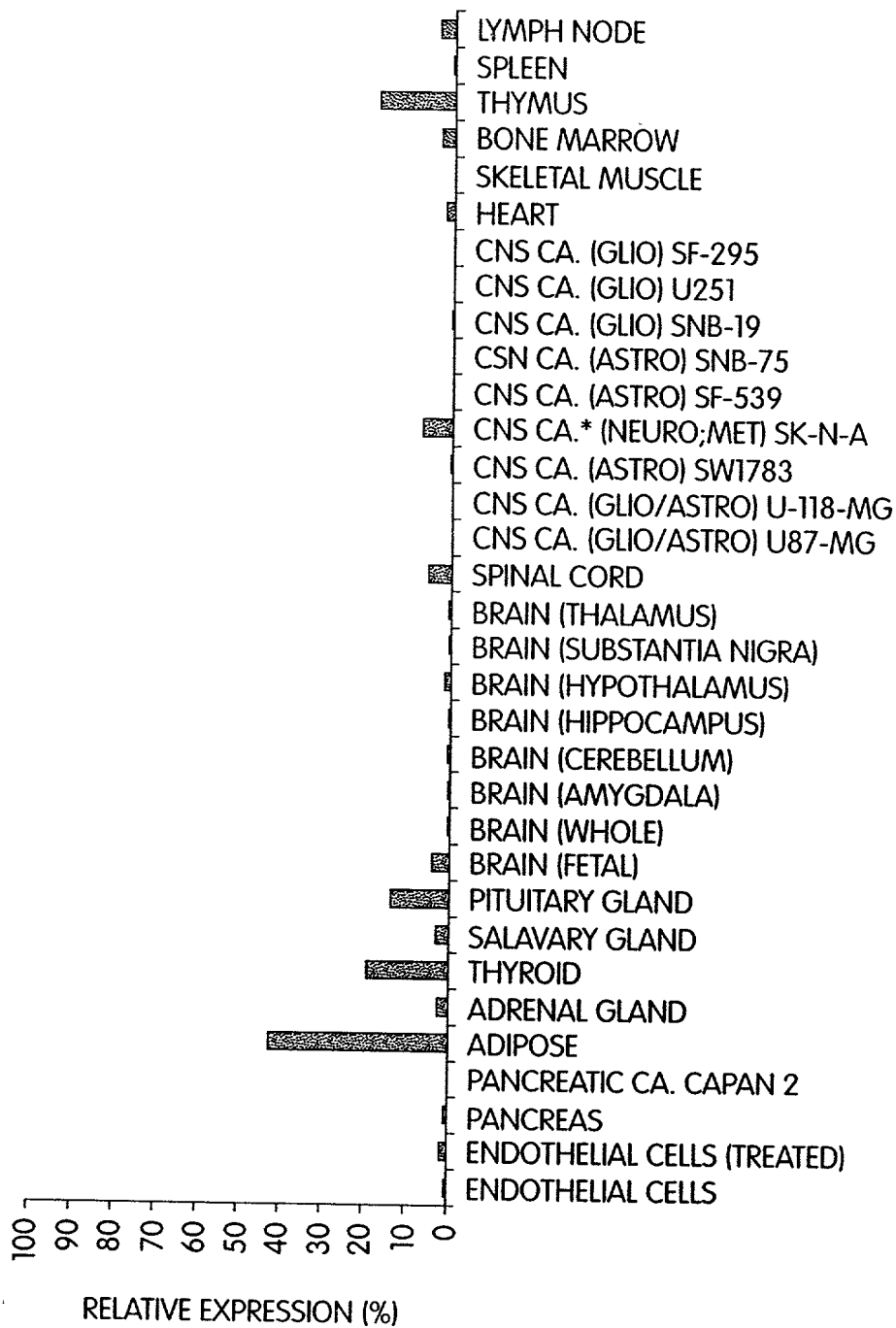
TISSUE SOURCE

LUNG CA. (SQUAM.) NCI-H596
LUNG CA. (SQUAM.) SW900
LUNG CA. (NON-S.CL) NCI-H522
LUNG CA. (NON-S.CELL) HOP-62
LUNG CA. (NON-S.CELL) NCI-H23
LUNG CA. (NON-SM. CELL) A-549
LUNG CA. (LARGE CELL)NCI-H460
LUNG CA. (S.CELL VAR.) SHP-77
LUNG CA. (SMALL CELL) NCI-H69
LUNG CA. (SMALL CELL) LX-1
LUNG (FETAL)
LUNG
LIVER CA. (HEPATOBLAST) HepG2
LIVER (FETAL)
LIVER
RENAL CA. TK-10
RENAL CA. UO-31
RENAL CA. ACHN
RENAL CA. RXF 393
RENAL CA. A498
RENAL CA. 786-0
KIDNEY (FETAL)
KIDNEY
TRACHEA
BLADDER
GASTRIC CA.* (LIVER MET) NCI-N87
COLON CA. HCC-2998
COLON CA. HCT-15
COLON CA. CaCo-2
COLON CA. HCT-116
COLON CA. HT29
COLON CA.* (SW480 MET)SW620
COLON CA. SW480
SMALL INTESTINE
STOMACH
COLON (ASCENDING)

MELANOMA UACC-257

MELANOMA SK-MEL-28

MELANOMA* (MET) SK-MEL-5

MELANOMA LOX IMVI

MELANOMA M14

MELANOMA UACC-62

MELANOMA* (MET) Hs688(B).T

MELANOMA Hs688(A).T

TESTIS

PROSTATE CA.* (BONE MET)PC-3

PROSTATE

PLANCENTA

UTERUS

MYOMETRIUM

OVARIAN CA.* (ASCITES) SK-OV-3

OVARIAN CA. IGROV-1

OVARIAN CA. OVCAR-8

OVARIAN CA. OVCAR-5

OVARIAN CA. OVCAR-4

OVARIAN CA. OVCAR-3

OVARY

BREAST CA. MDA-N

BREAST CA. BT-549

BREAST CA.* (PL. EFFUSION)...

BREAST CA.* (PL.EF) MDA-M...

BREAST CA.* (PL. EFFUSION)...

MAMMARY GLAND

TISSUE SOURCE

Fig. 6C

RELATIVE EXPRESSION (%)

100 90 80 70 60 50 40 30 20 10 0

LYMPH NODE
SPLEEN
THYMUS
BONE MARROW
SKELETAL MUSCLE
HEART
CNS CA. (GLIO) SF-295
CNS CA. (GLIO) U251
CNS CA. (GLIO) SNB-19
CSN CA. (ASTRO) SNB-75
CNS CA. (ASTRO) SF-539
CNS CA.* (NEURO;MET) SK-N-A
CNS CA. (ASTRO) SW1783
CNS CA. (GLIO/ASTRO) U-118-MG
CNS CA. (GLIO/ASTRO) U87-MG
SPINAL CORD
BRAIN (THALAMUS)
BRAIN (SUBSTANTIA NIGRA)
BRAIN (HYPOTHALAMUS)
BRAIN (HIPPOCAMPUS)
BRAIN (CEREBELLUM)
BRAIN (AMYGDALA)
BRAIN (WHOLE)
BRAIN (FETAL)
PITUITARY GLAND
SALAVARY GLAND
THYROID
ADRENAL GLAND
ADIPOSE
PANCREATIC CA. CAPAN 2
PANCREAS
ENDOTHELIAL CELLS (TREATED)
ENDOTHELIAL CELLS

TISSUE SOURCE

Fig. 7A

RELATIVE EXPRESSION (%)

100 90 80 70 60 50 40 30 20 10 0

LUNG CA. (SQUAM.) NCI-H596
LUNG CA. (SQUAM.) SW900
LUNG CA. (NON-S.CL) NCI-H522
LUNG CA. (NON-S.CELL) HOP-62
LUNG CA. (NON-S.CELL) NCI-23
LUNG CA. (NON-SM. CELL) A549
LUNG CA. (LARGE CELL)NCI-H460
LUNG CA. (S.CELL VAR.) SHP-77
LUNG CA. (SMALL CELL) NCI-H69
LUNG CA. (SMALL CELL) LX-1
LUNG (FETAL)
LUNG
LIVER CA. (HEPATOBLAST) HepG2
LIVER (FETAL)
LIVER
RENAL CA. TK-10
RENAL CA. UO-31
RENAL CA. ACHN
RENAL CA. RXF 393
RENAL CA. A498
RENAL CA. 786-0
KIDNEY (FETAL)
KIDNEY
TRACHEA
BLADDER
GASTRIC CA.* (LIVER MET) NCI-N87
COLON CA. HCC-2998
COLON CA. HCT-15
COLON CA. CaCo-2
COLON CA. HCT-116
COLON CA. HT29
COLON CA.* (SW480 MET)SW620
COLON CA. SW480
SMALL INTESTINE
STOMACH
COLON (ASCENDING)

TISSUE SOURCE

RELATIVE EXPRESSION (%)

100 90 80 70 60 50 40 30 20 10 0

Fig. 7B

MELANOMA UACC-257

MELANOMA SK-MEL-28

MELANOMA* (MET) SK-MEL-5

MELANOMA LOX IMVI

MELANOMA M14

MELANOMA UACC-62

MELANOMA* (MET) Hs688(B).T

MELANOMA Hs688(A).T

TESTIS

PROSTATE CA.* (BONE MET)PC-3

PROSTATE

PLANCENTA

UTERUS

MYOMETRIUM

OVARIAN CA.* (ASCITES) SK-OV-3

OVARIAN CA. IGROV-1

OVARIAN CA. OVCAR-8

OVARIAN CA. OVCAR-5

OVARIAN CA. OVCAR-4

OVARIAN CA. OVCAR-3

OVARY

BREAST CA. MDA-N

BREAST CA. BT-549

BREAST CA.* (PL. EFFUSION) T47D

BREAST CA.* (PL.EF) MDA-MB-231

BREAST CA.* (PL. EFFUSION) MCF-7

MAMMARY GLAND

TISSUE SOURCE

Fig. 7C

RELATIVE EXPRESSION (%)

100 90 80 70 60 50 40 30 20 10 0

Figure 8

>CG54007-01   20190 nt
ATGTGGGGGCTCCTGCTCGCCCTGGCCGCCTTCGCGCCGGCCGTCGGCCCGGCTCTGGGG
GCGCCCAGGAACTCGGTGCTGGGCCTCGCGCAGCCCGGGACCACCAAGGTCCCAGGCTCG
ACCCCGGCCCTGCATAGCAGCCCGGCACAGCCGCCGGCGGAGACAGCTAACGGGACCTCA
GAACAGCATGTCCGGATTCGAGTCATCAAGAAGAAAAAGGTCATTATGAAGAAGCGGAAG
AAGCTAACTCTAACTCGCCCCACCCCACTGGTGACTGCCGGGCCCCTTGTGACCCCCACT
CCAGCAGGGACCCTCGACCCCGCTGAGAAACAAGAAACAGGCTGTCCTCCTTTGGGTCTG
GAGTCCCTGCGAGTTTCAGATAGCCGGCTTGAGGCATCCAGCAGCCAGTCCTTTGGTCTT
GGACCACACCGAGGACGGCTCAACATTCAGTCAGGCCTGGAGGACGGCGATCTATATGAT
GGAGCCTGGTGTGCTGAGGAGCAGGACGCCGATCCATGGTTTCAGGTGGACGCTGGGCAC
CCCACCCGCTTCTCGGGTGTTATCACACAGGGCAGGAACTCTGTCTGGAGGTATGACTGG
GTCACATCATACAAGGTCCAGTTCAGCAATGACAGTCGGACCTGGTGGGGAAGTAGGAAC
CACAGCAGTGGGATGGACGCAGTATTTCCTGCCAATTCAGACCCAGAAACTCCAGTGCTG
AACCTCCTGCCGGAGCCCCAGGTGGCCCGCTTCATTCGCCTGCTGCCCCAGACCTGGCTC
CAGGGAGGCGCGCCTTGCCTCCGGGCAGAGATCCTGGCCTGCCCAGTCTCAGACCCCAAT
GACCTATTCCTTGAGGCCCCTGCGTCGGGATCCTCTGACCCTCTAGACTTTCAGCATCAC
AATTACAAGGCCATGAGGAAGCTGATGAAGCAGGTACAAGAGCAATGCCCCAACATCACC
CGCATCTACAGCATTGGGAAGAGCTACCAGGGCCTGAAGCTGTATGTGATGGAAATGTCG
GACAAGCCTGGGGAGCATGAGCTGGGGGAGCCTGAGGTGCGCTACGTGGCTGGCATGCAT
GGGAACGAGGCCCTGGGGCGGGAGTTGCTTCTGCTCCTGATGCAGTTCCTGTGCCATGAG
TTCCTGCGAGGGAACCCACGGGTGACCCGGCTGCTCTCTGAGATGCGCATTCACCTGCTG
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GGACAGGAAGTGCAGTTTGCTGGCAGCGTGGCATCGTGTTAGAGCCGGTGGGAGGAGCCT
CCATTGCAGTCTAGGTGGTGGTCCGTGGCGCTGCCCCAGAGCTATCCTCAGGAGAGACTC
ACGTGAGGCAGGTGCAGGAGCTGTCCTGGCATAGAAGCTTCATGTTCCATGGAGCTCATA
ACCCTTGTAATAGCTCCATAAGCAGAGCTTCCAAAGGGTCTACCAAAGACAAGCCCAATA
ACCTGGGAAAGCCCAAGGATAGATAAGCCTTCCTACCAGGTATTTATCATTTTCTTAGTC
CAGATGTGATTTGTCAATCAGGATTTCTTTTTTTTTTTTCTTCCAGAAGTAGTGTCACCT
AGGAACACAGTAGACCTACCACTTTGCTCAGGTTTGCAGGGCAACAGAGCCAGCAAGTTA
GCTAAACAGCACATTATCCTGCCGAAGGGGAAGGGCTCTGATAACCTCTTCCCACACAGG
TGCGCATGGGCATTGCAGGAGTGGTGAGGGACAAGGACACGGAGCTTGGGATTGCTGACG
CTGTCATTGCCGTGGATGGGATTAACCATGACGTGACCACGGGTGTGTTTGACCGGGAGG
GCAAGGGAAGGGGCTGGAGGGCTGGAGGCTCGGGAAGAAGCAGAAGATCATTAATTGGGT
CCTGATCGTGCCCTTCACTCTCCTCAGCGTGGGGCGGGGATTATTGGCGTCTGCTGACCC
CAGGGGACTACATGGTGACTGCCAGTGCCGAGGGCTACCATTCAGTGACACGGAACTGTC
GGGTCACCTTTGAAGAGGGCCCCTTCCCCTGCAATTTCGTGCTCACCAAGACTCCCAAAC
AGAGGCTGCGCGAGCTGCTGGCAGCTGGGGCCAAGGTGCCCCCGGACCTTCGCAGGCGCC
TGGAGCGGCTAAGGGGACAGAAGGATTGATACCTGCGGTTTAAGAGCCCTAGGGCAGGCT
GGACCTGTCAAGACGGGAAGGGGAAGAGTAGAGAGGGAGGGACAAAGTGAGGAAAAGGTG
CTCATTAAAGCTACCGGGCACCTTAGCTCATCTTCGTGTTGTCTCTGTGCCCCAGGTCCT
CCCCCCGGGGGCGGGCCTCGGCCCAGCCCTCAGTTCCTATTCTGCACACTTGCACACTCT
CATCAGTTGGCTTCTGGACACATTGTGTGAAAAGAGGATCCCACCTGGGCTCTTCTTGAA
CCAAGGGCCTGGCAGAGCAACTCATTTCTTCTGATCAGCTTCTGCTACAGGTACCATTAC
ACTGCTGCCAGGCATTCTGTAAGCGCCTGCTCATTGCCAGGTGTGCAAGGAATCAGGATC
AGCCGTGCCTGCACTCAAACTCCTGGGGCTCCTAGTCAAGGGAAAGGACAGTTCGGTACA
TTGTGAGACATGCTAGGGTGGAGGCCAGGTGCCGTGAGAGTGCAGGGGAGCTGCACACGT
GAAATACAGCACTGCACATCAACAGGACTGGGGCAGTCAAGGATGCAATAGAAGTAGTGG
CTCTAGAAGTTCAGGCGGGAGGTGGGCAGGGTGTGGAGTATGGACAGGGATGGCTCCAAG
GAGGAGGGTCAGCCAAAGGTGGGTCAGCTGAGAACATTTGAATTTGCTTCAGCCATTCTC
AGAGTATTGATAACTGATAGGCTTTGCTGAGTTTCTATCAGACTGAAGGGGAAGTTGTGT
ATCAGTCTGTGTCTTGCCAGGTAAACAACCCATTCTAGGCACTTAAAGTGGAGGGAAATT
TAATGCTGGAAATTGGATAGGAAGGTGTTGGAAGAGCTGGATGAGGCCGGGTGTGGTGGC
TCACACCTGTAATCCCAGCACTTTGGGAGGCTGAGGTGGGAGGATTGCTTGAGCCCAGGA
GTTTGAGACCAGCCTGGATAACATAGCCAAACCCCGCCTCTACAAAAATAAGAAATAAGA
AACATAGCCAGCTGTAGTGGCGCATGGCTAAGGGAGGCAGAGGCAGGAGGATCACTGGAG
CCTGGGAGGTGGAGGCTGCAGAGGCAGCAGTGAGCCATGATGGCGCCACTATACTCCAAC
CTGGATGGTCATAACAAAATAAACAAAAA (SEQ ID NO:3)

FIG 9

>CG54007-04
ATGTGGGGGGCTCCTGCTCGCCCTGGCCGCCTTCGCGCCGGCCGTCGGCCCGGCTCTGGGG   60
GCGCCCAGGAACTCGGTGCTGGGCCTCGCGCAGCCCGGGACCACCAAGGTCCCAGGCTCG   120
ACCCCGGCCCTGCATAGCAGCCCGGCACAGCCGCCGGCGGAGACAGCTAACGGGACCTCA   180
GAACAGCATGTCCGGATTCGAGTCATCAAGAAGAAAAAGGTCATTATGAAGAAGCGGAAG   240
AAGCTAACTCTAACTCGCCCCACCCCACTGGTGACTGCCGGGCCCCTTGTGACCCCCACT   300
CCAGCAGGGACCCTCGACCCCGCTGAGAAACAAGAAACAGGCTGTCCTCCTTTGGGTCTG   360
GAGTCCCTGCGAGTTTCAGATAGCCGGCTTGAGGCATCCAGCAGCCAGTCCTTTGGTCTT   420
GGACCACACCGAGGACGGCTCAACATTCAGTCAGGCCTGGAGGACGGCGATCTATATGAT   480
GGAGCCTGGTGTGCTGAGGAGCAGGACGCCGATCCATGGTTTCAGGTGGACGCTGGGCAC   540
CCCACCCGCTTCTCGGGTGTTATCACACAGGGCAGGAACTCTGTCTGGAGGTATGACTGG   600
GTCACATCATACAAGGTCCAGTTCAGCAATGACAGTCGGACCTGGTGGGGAAGTAGGAAC   660
CACAGCAGTGGGATGGACGCAGTATTTCCTGCCAATTCAGACCCAGAAACTCCAGTGCTG   720
AACCTCCTGCCGGAGCCCCAGGTGGCCCGCTTCATTCGCCTGCTGCCCCAGACCTGGCTC   780
CAGGGAGGCGCGCCTTGCCTCCGGGCAGAGATCCTGGCCTGCCCAGTCTCAGACCCCAAT   840
GACCTATTCCTTGAGGCCCCTGCGTCGGGATCCTCTGACCCTCTAGACTTTCAGCATCAC   900
AATTACAAGGCCATGAGGAAGCTGATGAAGCAGGTACAAGAGCAATGCCCCAACATCACC   960
CGCATCTACAGCATTGGGAAGAGCTACCAGGGCCTGAAGCTGTATGTGATGGAAATGTCG   1020
GACAAGCCTGGGGAGCATGAGCTGGGGGAGCCTGAGGTGCGCTACGTGGCTGGCATGCAT   1080
GGGAACGAGGCCCTGGGGCGGGAGTTGCTTCTGCTCCTGATGCAGTTCCTGTGCCATGAG   1140
TTCCTGCGAGGGAACCCACGGGTGACCCGGCTGCTCTCTGAGATGCGCATTCACCTGCTG   1200
CCCTCCATGAACCCTGATGGCTATGAGATCGCCTACCACGGGGTTCAGAGCTGGTGGGC   1260
TGGGCCGAGGGCCGCTGGAACAACCAGAGCATCGATCTTAACCATAATTTTGCTGACCTC   1320
AACACCACTGTGGGAAGCACAGGACGATGGGAAGGTGCCCCACATCGTCCCCAACCAT   1380
CACCTGCCATTGCCCACTTACTACACCCTGCCCAATGCCACCGTGGCTCCTGAAACGCGG   1440
GCAGTAATCAAGTGGATGAAGCGGATCCCCTTTGTGCTAAGTGCCAACCTCCACGGGGGT   1500
GAGCTCGTGGTGTCCTACCCATTCGACATGGTGACTGCCAGTGCCGAGGGCTACCATTCA   1560
GTGACACGGAACTGTCGGGTCACCTTTGAAGAGGGCCCCTTCCCCTGCAATTTCGTGCTC   1620
ACCAAGACTCCCAAACAGAGGCTGCGCGAGCTGCTGGCAGCTGGGGCCAAGGTGCCCCCG   1680
GACCTTCGCAGGCGCCTGGAGCGGCTAAGGGGACAGAAGGAT**TGA**   (SEQ ID NO:5)1725

FIG. 10

>CG54007-04
MWGLLLALAAFAPAVGPALGAPRNSVLGLAQPGTTKVPGSTPALHSSPAQPPAETANGTS   60
EQHVRIRVIKKKKVIMKKRKKLTLTRPTPLVTAGPLVTPTPAGTLDPAEKQETGCPPLGL   120
ESLRVSDSRLEASSSQSFGLGPHRGRLNIQSGLEDGDLYDGAWCAEEQDADPWFQVDAGH   180
PTRFSGVITQGRNSVWRYDWVTSYKVQFSNDSRTWWGSRNHSSGMDAVFPANSDPETPVL   240
NLLPEPQVARFIRLLPQTWLQGGAPCLRAEILACPVSDPNDLFLEAPASGSSDPLDFQHH   300
NYKAMRKLMKQVQEQCPNITRIYSIGKSYQGLKLYVMEMSDKPGEHELGEPEVRYVAGMH   360
GNEALGRELLLLLMQFLCHEFLRGNPRVTRLLSEMRIHLLPSMNPDGYEIAYHRGSELVG   420
WAEGRWNNQSIDLNHNFADLNTPLWEAQDDGKVPHIVPNHHLPLPTYYTLPNATVAPETR   480
AVIKWMKRIPFVLSANLHGGELVVSYPFDMVTASAEGYHSVTRNCRVTFEEGPFPCNFVL   540
TKTPKQRLRELLAAGAKVPPDLRRRLERLRGQKD   (SEQ ID NO:6)574

FIG. 11

>CG54007-05
ATGTGGGGGGCTCCTGCTCGCCCTGGCCGCCTTCGCGCCGGCCGTCGGCCCGGCTCTGGGG 60
GCGCCCAGGAACTCGGTGCTGGGCCTCGCGCAGCCCGGGACCACCAAGGTCCCAGGCTCG 120
ACCCCGGCCCTGCATAGCAGCCCGGCACAGCCGCCGGCGGAGACAGCTAACGGGACCTCA 180
GAACAGCATGTCCGGATTCGAGTCATCAAGAAGAAAAAGGTCATTATGAAGAAGCGGAAG 240
AAGCTAACTCTAACTCGCCCCACCCCACTGGTGACTGCCGGGCCCCTTGTGACCCCCACT 300
CCAGCAGGGACCCTCGACCCCGCTGAGAAACAAGAAACAGGCTGTCCTCCTTTGGGTCTG 360
GAGTCCCTGCGAGTTTCAGATAGCCGGCTTGAGGCATCCAGCAGCCAGTCCTTTGGTCTT 420
GGACCACACCGAGGACGGCTCAACATTCAGTCAGGCCTGGAGGACGGCGATCTATATGAT 480
GGAGCCTGGTGTGCTGAGGAGCAGGACGCCGATCCATGGTTTCAGGTGGACGCTGGGCAC 540
CCCACCCGCTTCTCGGGTGTTATCACACAGGGCAGAGATCCTGGCCTGCCCAGTCTCAGA 600
CCCCAA**TGA**CCTATTCCTTGAGGCCCCTGCGTCGGGATCCTCTGACCCTCTAGACTTTCA 660
GCATCACAATTACAAGGCCATGAGGAAGCTGATGAAGCAGGTACAAGAGCAATGCCCCAA 720
CATCACCCGCATCTACAGCATTGGGAAGAGCTACCAGGGCCTGAAGCTGTATGTGATGGA 780
AATGTCGGACAAGCCTGGGGAGCATGAGCTGGGGGAGCCTGAGGTGCGCTACGTGGCTGG 840
CATGCATGGGAACGAGGCCCTGGGGCGGGAGTTGCTTCTGCTCCTGATGCAGTTCCTGTG 900
CCATGAGTTCCTGCGAGGGAACCCACGGGTGACCCGGCTGCTCTCTGAGATGCGCATTCA 960
CCTGCTGCCCTCCATGAACCCTGATGGCTATGAGATCGCCTACCACCGGGGTTCAGAGCT 1020
GGTGGGCTGGGCCGAGGGCCGCTGGAACAACCAGAGCATCGATCTTAACCATAATTTTGC 1080
TGACCTCAACACACCACTGTGGGAAGCACAGGACGATGGGAAGGTGCCCCACATCGTCCC 1140
CAACCATCACCTGCCATTGCCCACTTACTACACCCTGCCCAATGCCACCGTGGCTCCTGA 1200
AACGCGGGCAGTAATCAAGTGGATGAAGCGGATCCCCTTTGTGCTAAGTGCCAACCTCCA 1260
CGGGGGTGAGCTCGTGGTGTCCTACCCATTCGACATGACTCGCACCCCGTGGGCTGCCCG 1320
CGAGCTCACGCCCACACCAGATGATGCTGTGTTTCGCTGGCTCAGCACTGTCTATGCTGG 1380
CAGTAATCTGGCCATGCAGGACACCAGCCGCCGACCCTGCCACAGCCAGGACTTCTCCGT 1440
GCACGGCAACATCATCAACGGGGCTGACTGGCACACGGTCCCCGGGAGCATGAATGACTT 1500
CAGCTACCTACACACCAACTGCTTTGAGGTCACTGTGGAGCTGTCCTGTGACAAGTTCCC 1560
TCACGAGAATGAATTGCCCCAGGAGTGGGAGAACAACAAAGACGCCCTCCTCACCTACCT 1620
GGAGCAGGTGCGCATGGGCATTGCAGGAGTGGTGAGGGACAAGGACACGGAGCTTGGGAT 1680
TGCTGACGCTGTCATTGCCGTGGATGGGATTAACCATGACGTGACCACGGCGTGGGGCGG 1740
GGATTATTGGCGTCTGCTGACCCCCAGGGGACTACATGGTGACTGCCAGTGCCGAGGGCTA 1800
CCATTCAGTGACACGGAACTGTCGGGTCACCTTTGAAGAGGGCCCCTTCCCCTGCAATTT 1860
CGTGCTCACCAAGACTCCCAAACAGAGGCTGCGCGAGCTGCTGGCAGCTGGGGCCAAGGT 1920
GCCCCCGGACCTTCGCAGGCGCCTGGAGCGGCTAAGGGGACAGAAGGATTGA   (SEQ ID NO:7)1972

FIG. 12

>CG54007-05
MWGLLLALAAFAPAVGPALGAPRNSVLGLAQPGTTKVPGSTPALHSSPAQPPAETANGTS   60
EQHVRIRVIKKKKVIMKKRKKLTLTRPTPLVTAGPLVTPTPAGTLDPAEKQETGCPPLGL   120
ESLRVSDSRLEASSSQSFGLGPHRGRLNIQSGLEDGDLYDGAWCAEEQDADPWFQVDAGH   180
PTRFSGVITQGRDPGLPSLRPQ   (SEQ ID NO:8)202

FIG. 13

>CG54007-06

```
ATGTGGGGGCTCCTGCTCGCCCTGGCCGCCTTCGCGCCGGCCGTCGGCCCGGCTCTGGGG        60
GCGCCCAGGAACTCGGTGCTGGGCCTCGCGCAGCCCGGGACCACCAAGGTCCCAGGCTCG       120
ACCCCGGCCCTGCATAGCAGCCCGGCACAGCCGCCGGCGGAGACAGCTAACGGGACCTCA       180
GAACAGCATGTCCGGATTCGTGTCATCAAGAAGAAAAAGGTCATTATGAAGAAGCGGAAG       240
AAGCTAACTCTAACTCGCCCCACCCCACTGGTGACTGCCGGGCCCCTTGTGACCCCCACT       300
CCAGCAGGGACCCTCGACCCCGCTGAGAAACAAGAAACAGGCTGTCCTCCTTTGGGTCTG       360
GAGTCCCTGCGAGTTTCAGATAGCCGGCTTGAGGCATCCAGCAGCCAGTCCTTTGGTCTT       420
GGACCACACCGAGGACGGCTCAACATTCAGTCAGGCCTGGAGGACGGCGATCTATATGAT       480
GGAGCCTGGTGTGCTGAGGAGCAGGACGCCGATCCATGGTTTCAGGTGGACGCTGGGCAC       540
CCCACCCGCTTCTCGGGTGTTATCACACAGGGCAGGAACTCTGTCTGGAGGTATGACTGG       600
GTCACATCATACAAGGTCCAGTTCAGCAATGACAGTCGGACCTGGTGGGGAAGTAGGAAC       660
CACAGCAGTGGGATGGACGCAGTATTTCCTGCCAATTCAGACCCAGAAACTCCAGTGCTG       720
AACCTCCTGCCGGAGCCCCAGGTGGCCCGCTTCATTCGCCTGCTGCCCCAGACCTGGCTC       780
CAGGGAGGCGCGCCTTGCCTCCGGGCAGAGATCCTGGCCTGCCCAGTCTCAGACCCCAAT       840
GACCTATTCCTTGAGGCCCCTGCGTCGGGATCCTCTGACCCTCTAGACTTTCAGCATCAC       900
AATTACAAGGCCATGAGGAAGCTGATGAAGCAGGTACAAGAGCAATGCCCCAACATCACC       960
CGCATCTACAGCATTGGGAAGAGCTACCAGGGCCTGAAGCTGTATGTGATGGAAATGTCG      1020
GACAAGCCTGGGGAGCATGAGCTGGGGGAGCCTGAGGTGCGCTACGTGGCTGGCATGCAT      1080
GGGAACGAGGCCCTGGGGCGGGAGTTGCTTCTGCTCCTGATGCAGTTCCTGTGCCATGAG      1140
TTCCTGCGAGGGAACCCACGGGTGACCCGGCTGCTCTCTGAGATGCGCATTCACCTGCTG      1200
CCCTCCATGAACCCTGATGGCTATGAGATCGCCTACCACCGGGGTTCAGAGCTGGTGGGC      1260
TGGGCCGAGGGCCGCTGGAACAACCAGAGCATCGATCTTAACCATAATTTTGCTGACCTC      1320
AACACACCACTGTGGGAAGCACAGGACGATGGGAAGGTGCCCCACATCGTCCCCAACCAT      1380
CACCTGCCATTGCCCACTTACTACACCCTGCCCAATGCCACCGTGGCTCCTGAAACGCGG      1440
GCAGTAATCAAGTGGATGAAGCGGATCCCCTTTGTGCTAAGTGCCAACCTCCACGGGGGT      1500
GAGCTCGTGGTGTCCTACCCATTCGACATGACTCGCACCCCGTGGGCTGCCCGCGAGCTC      1560
ACGCCCACACCAGATGATGCTGTGTTTCGCTGGCTCAGCACTGTCTATGCTGGCAGTAAT      1620
CTGGCCATGCAGGACACCAGCCGCCGACCCTGCCACAGCCAGGACTTCTCCGTGCACGGC      1680
AACATCATCAACGGGGCTGACTGGCACACGGTCCCCGGGAGCATGAATGACTTCAGCTAC      1740
CTACACCAACTGCTTTGAGGTCACTGTGGAGCTGTCCTGTGACAAGTTCCCTCACGAG      1800
AATGAATTGCCCCAGGAGTGGGAGAACAACAAAGACGCCCTCCTCACCTACCTGGAGCAG      1860
GTGCGCATGGGCATTGCAGGAGTGGTGAGGGACAAGGACACGGAGCTTGGGATTGCTGAC      1920
GCTGTCATTGCCGTGGATGGGATTAACCATGACGTGACCACGGCGTGGGGCGGGGATTAT      1980
TGGCGTCTGCTGACCCCAGGGGACTACATGGTGACTGCCAGTGCCGAGGGCTACCATTCA      2040
GTGACACGGAACTGTCGGGTCACCTTTGAAGAGGGCCCCTTCCCCTGCAATTTCGTGCTC      2100
ACCAAGACTCCCAAACAGAGGCTGCGCGAGCTGCTGGCAGCTGGGGCCAAGGTGCCCCCG      2160
GACCTTCGCAGGCGCCTGGAGCGGCTAAGGGGACAGAAGGATTGA (SEQ ID NO:4)      2205
```

Figure 14.

```
>ptnr:SPTREMBL-ACC:Q9NUB5 DJ860F19.3 (NOVEL PROTEIN (ORTHOLOG OF MOUSE
        METALLOCARBOXYPEPTIDASE CPX-1)) - Homo sapiens (Human), 734 aa.
        Length = 734

 Score = 2735 (962.8 bits), Expect = 0.0, Sum P(2) = 0.0
 Identities = 510/510 (100%), Positives = 510/510 (100%)

Query:     1 MWGLLLALAAFAPAVGPALGAPRNSVLGLAQPGTTKVPGSTPALHSSPAQPPAETANGTS 60
             MWGLLLALAAFAPAVGPALGAPRNSVLGLAQPGTTKVPGSTPALHSSPAQPPAETANGTS
Sbjct:     1 MWGLLLALAAFAPAVGPALGAPRNSVLGLAQPGTTKVPGSTPALHSSPAQPPAETANGTS 60

Query:    61 EQHVRIRVIKKKKVIMKKRKKLTLTRPTPLVTAGPLVTPTPAGTLDPAEKQETGCPPLGL 120
             EQHVRIRVIKKKKVIMKKRKKLTLTRPTPLVTAGPLVTPTPAGTLDPAEKQETGCPPLGL
Sbjct:    61 EQHVRIRVIKKKKVIMKKRKKLTLTRPTPLVTAGPLVTPTPAGTLDPAEKQETGCPPLGL 120

Query:   121 ESLRVSDSRLEASSSQSFGLGPHRGRLNIQSGLEDGDLYDGAWCAEEQDADPWFQVDAGH 180
             ESLRVSDSRLEASSSQSFGLGPHRGRLNIQSGLEDGDLYDGAWCAEEQDADPWFQVDAGH
Sbjct:   121 ESLRVSDSRLEASSSQSFGLGPHRGRLNIQSGLEDGDLYDGAWCAEEQDADPWFQVDAGH 180

Query:   181 PTRFSGVITQGRNSVWRYDWVTSYKVQFSNDSRTWWGSRNHSSGMDAVFPANSDPETPVL 240
             PTRFSGVITQGRNSVWRYDWVTSYKVQFSNDSRTWWGSRNHSSGMDAVFPANSDPETPVL
Sbjct:   181 PTRFSGVITQGRNSVWRYDWVTSYKVQFSNDSRTWWGSRNHSSGMDAVFPANSDPETPVL 240

Query:   241 NLLPEPQVARFIRLLPQTWLQGGAPCLRAEILACPVSDPNDLFLEAPASGSSDPLDFQHH 300
             NLLPEPQVARFIRLLPQTWLQGGAPCLRAEILACPVSDPNDLFLEAPASGSSDPLDFQHH
Sbjct:   241 NLLPEPQVARFIRLLPQTWLQGGAPCLRAEILACPVSDPNDLFLEAPASGSSDPLDFQHH 300

Query:   301 NYKAMRKLMKQVQEQCPNITRIYSIGKSYQGLKLYVMEMSDKPGEHELGEPEVRYVAGMH 360
             NYKAMRKLMKQVQEQCPNITRIYSIGKSYQGLKLYVMEMSDKPGEHELGEPEVRYVAGMH
Sbjct:   301 NYKAMRKLMKQVQEQCPNITRIYSIGKSYQGLKLYVMEMSDKPGEHELGEPEVRYVAGMH 360

Query:   361 GNEALGRELLLLLMQFLCHEFLRGNPRVTRLLSEMRIHLLPSMNPDGYEIAYHRGSELVG 420
             GNEALGRELLLLLMQFLCHEFLRGNPRVTRLLSEMRIHLLPSMNPDGYEIAYHRGSELVG
Sbjct:   361 GNEALGRELLLLLMQFLCHEFLRGNPRVTRLLSEMRIHLLPSMNPDGYEIAYHRGSELVG 420

Query:   421 WAEGRWNNQSIDLNHNFADLNTPLWEAQDDGKVPHIVPNHHLPLPTYYTLPNATVAPETR 480
             WAEGRWNNQSIDLNHNFADLNTPLWEAQDDGKVPHIVPNHHLPLPTYYTLPNATVAPETR
Sbjct:   421 WAEGRWNNQSIDLNHNFADLNTPLWEAQDDGKVPHIVPNHHLPLPTYYTLPNATVAPETR 480

Query:   481 AVIKWMKRIPFVLSANLHGGELVVSYPFDM 510    (Seq ID NO:45)
             AVIKWMKRIPFVLSANLHGGELVVSYPFDM
Sbjct:   481 AVIKWMKRIPFVLSANLHGGELVVSYPFDM 510


 Score = 341 (120.0 bits), Expect = 0.0, Sum P(2) = 0.0
 Identities = 67/69 (97%), Positives = 67/69 (97%)

Query:   507 PFD-MVTASAEGYHSVTRNCRVTFEEGPFPCNFVLTKTPKQRLRELLAAGAKVPPDLRRR 565
             P D MVTASAEGYHSVTRNCRVTFEEGPFPCNFVLTKTPKQRLRELLAAGAKVPPDLRRR
Sbjct:   666 PGDYMVTASAEGYHSVTRNCRVTFEEGPFPCNFVLTKTPKQRLRELLAAGAKVPPDLRRR 725

Query:   566 LERLRGQKD 574 (SEQ ID NO:46)
             LERLRGQKD     (SEQ ID NO:41)
Sbjct:   726 LERLRGQKD 734 (SEQ ID NO:42)
```

Figure 15

```
>ptnr:SPTREMBL-ACC:Q9NUB5 DJ860F19.3 (NOVEL PROTEIN (ORTHOLOG OF MOUSE
        METALLOCARBOXYPEPTIDASE CPX-1)) - Homo sapiens (Human), 734 aa.
        Length = 734

 Score = 1005 (353.8 bits), Expect = 4.4e-101, P = 4.4e-101
 Identities = 192/193 (99%), Positives = 193/193 (100%)

Query:     1 MWGLLLALAAFAPAVGPALGAPRNSVLGLAQPGTTKVPGSTPALHSSPAQPPAETANGTS 60
             MWGLLLALAAFAPAVGPALGAPRNSVLGLAQPGTTKVPGSTPALHSSPAQPPAETANGTS
Sbjct:     1 MWGLLLALAAFAPAVGPALGAPRNSVLGLAQPGTTKVPGSTPALHSSPAQPPAETANGTS 60

Query:    61 EQHVRIRVIKKKKVIMKKRKKLTLTRPTPLVTAGPLVTPTPAGTLDPAEKQETGCPPLGL 120
             EQHVRIRVIKKKKVIMKKRKKLTLTRPTPLVTAGPLVTPTPAGTLDPAEKQETGCPPLGL
Sbjct:    61 EQHVRIRVIKKKKVIMKKRKKLTLTRPTPLVTAGPLVTPTPAGTLDPAEKQETGCPPLGL 120

Query:   121 ESLRVSDSRLEASSSQSFGLGPHRGRLNIQSGLEDGDLYDGAWCAEEQDADPWFQVDAGH 180
             ESLRVSDSRLEASSSQSFGLGPHRGRLNIQSGLEDGDLYDGAWCAEEQDADPWFQVDAGH
Sbjct:   121 ESLRVSDSRLEASSSQSFGLGPHRGRLNIQSGLEDGDLYDGAWCAEEQDADPWFQVDAGH 180

Query:   181 PTRFSGVITQGRD 193 (SEQ ID NO:47)
             PTRFSGVITQGR+    (SEQ ID NO:43)
Sbjct:   181 PTRFSGVITQGRN 193 (SEQ ID NO:44)
```

Figure 16

```
>ptnr:SPTREMBL-ACC:Q9NUB5 DJ860F19.3 (NOVEL PROTEIN (ORTHOLOG OF MOUSE
         METALLOCARBOXYPEPTIDASE CPX-1)) - Homo sapiens (Human), 734 aa.
         Length = 734

 Score = 3952 (1391.2 bits), Expect = 0.0, P = 0.0
 Identities = 734/734 (100%), Positives = 734/734 (100%)

Query:     1 MWGLLLALAAFAPAVGPALGAPRNSVLGLAQPGTTKVPGSTPALHSSPAQPPAETANGTS 60
             MWGLLLALAAFAPAVGPALGAPRNSVLGLAQPGTTKVPGSTPALHSSPAQPPAETANGTS
Sbjct:     1 MWGLLLALAAFAPAVGPALGAPRNSVLGLAQPGTTKVPGSTPALHSSPAQPPAETANGTS 60

Query:    61 EQHVRIRVIKKKKVIMKKRKKLTLTRPTPLVTAGPLVTPTPAGTLDPAEKQETGCPPLGL 120
             EQHVRIRVIKKKKVIMKKRKKLTLTRPTPLVTAGPLVTPTPAGTLDPAEKQETGCPPLGL
Sbjct:    61 EQHVRIRVIKKKKVIMKKRKKLTLTRPTPLVTAGPLVTPTPAGTLDPAEKQETGCPPLGL 120

Query:   121 ESLRVSDSRLEASSSQSFGLGPHRGRLNIQSGLEDGDLYDGAWCAEEQDADPWFQVDAGH 180
             ESLRVSDSRLEASSSQSFGLGPHRGRLNIQSGLEDGDLYDGAWCAEEQDADPWFQVDAGH
Sbjct:   121 ESLRVSDSRLEASSSQSFGLGPHRGRLNIQSGLEDGDLYDGAWCAEEQDADPWFQVDAGH 180

Query:   181 PTRFSGVITQGRNSVWRYDWVTSYKVQFSNDSRTWWGSRNHSSGMDAVFPANSDPETPVL 240
             PTRFSGVITQGRNSVWRYDWVTSYKVQFSNDSRTWWGSRNHSSGMDAVFPANSDPETPVL
Sbjct:   181 PTRFSGVITQGRNSVWRYDWVTSYKVQFSNDSRTWWGSRNHSSGMDAVFPANSDPETPVL 240

Query:   241 NLLPEPQVARFIRLLPQTWLQGGAPCLRAEILACPVSDPNDLFLEAPASGSSDPLDFQHH 300
             NLLPEPQVARFIRLLPQTWLQGGAPCLRAEILACPVSDPNDLFLEAPASGSSDPLDFQHH
Sbjct:   241 NLLPEPQVARFIRLLPQTWLQGGAPCLRAEILACPVSDPNDLFLEAPASGSSDPLDFQHH 300

Query:   301 NYKAMRKLMKQVQEQCPNITRIYSIGKSYQGLKLYVMEMSDKPGEHELGEPEVRYVAGMH 360
             NYKAMRKLMKQVQEQCPNITRIYSIGKSYQGLKLYVMEMSDKPGEHELGEPEVRYVAGMH
Sbjct:   301 NYKAMRKLMKQVQEQCPNITRIYSIGKSYQGLKLYVMEMSDKPGEHELGEPEVRYVAGMH 360

Query:   361 GNEALGRELLLLLMQFLCHEFLRGNPRVTRLLSEMRIHLLPSMNPDGYEIAYHRGSELVG 420
             GNEALGRELLLLLMQFLCHEFLRGNPRVTRLLSEMRIHLLPSMNPDGYEIAYHRGSELVG
Sbjct:   361 GNEALGRELLLLLMQFLCHEFLRGNPRVTRLLSEMRIHLLPSMNPDGYEIAYHRGSELVG 420

Query:   421 WAEGRWNNQSIDLNHNFADLNTPLWEAQDDGKVPHIVPNHHLPLPTYYTLPNATVAPETR 480
             WAEGRWNNQSIDLNHNFADLNTPLWEAQDDGKVPHIVPNHHLPLPTYYTLPNATVAPETR
Sbjct:   421 WAEGRWNNQSIDLNHNFADLNTPLWEAQDDGKVPHIVPNHHLPLPTYYTLPNATVAPETR 480

Query:   481 AVIKWMKRIPFVLSANLHGGELVVSYPFDMTRTPWAARELTPTPDDAVFRWLSTVYAGSN 540
             AVIKWMKRIPFVLSANLHGGELVVSYPFDMTRTPWAARELTPTPDDAVFRWLSTVYAGSN
Sbjct:   481 AVIKWMKRIPFVLSANLHGGELVVSYPFDMTRTPWAARELTPTPDDAVFRWLSTVYAGSN 540

Query:   541 LAMQDTSRRPCHSQDFSVHGNIINGADWHTVPGSMNDFSYLHTNCFEVTVELSCDKFPHE 600
             LAMQDTSRRPCHSQDFSVHGNIINGADWHTVPGSMNDFSYLHTNCFEVTVELSCDKFPHE
Sbjct:   541 LAMQDTSRRPCHSQDFSVHGNIINGADWHTVPGSMNDFSYLHTNCFEVTVELSCDKFPHE 600

Query:   601 NELPQEWENNKDALLTYLEQVRMGIAGVVRDKDTELGIADAVIAVDGINHDVTTAWGGDY 660
             NELPQEWENNKDALLTYLEQVRMGIAGVVRDKDTELGIADAVIAVDGINHDVTTAWGGDY
Sbjct:   601 NELPQEWENNKDALLTYLEQVRMGIAGVVRDKDTELGIADAVIAVDGINHDVTTAWGGDY 660

Query:   661 WRLLTPGDYMVTASAEGYHSVTRNCRVTFEEGPFPCNFVLTKTPKQRLRELLAAGAKVPP 720
             WRLLTPGDYMVTASAEGYHSVTRNCRVTFEEGPFPCNFVLTKTPKQRLRELLAAGAKVPP
Sbjct:   661 WRLLTPGDYMVTASAEGYHSVTRNCRVTFEEGPFPCNFVLTKTPKQRLRELLAAGAKVPP 720

Query:   721 DLRRRLERLRGQKD 734 (SEQ ID NO:2)
             DLRRRLERLRGQKD
Sbjct:   721 DLRRRLERLRGQKD 734
```

Fig. 17

A.

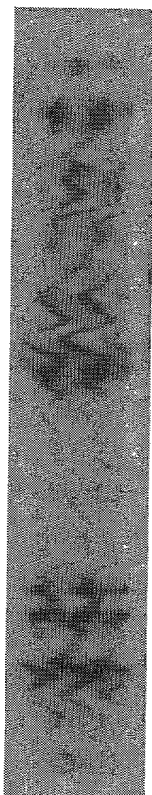| kDa	
116	
98	
66	
55	
	←
36	
30	
21	
16	
6	

B.

KKLTLTRPTPLVTAGPL
| | | | | | | | | | ∘ | | | | ∘ | | | |
KKLTLTRPPPLV-AGPL

Figure 18 ClustalW alignment of CG54007-01, CG54007-04 and CG54007-05 proteins of the present invention.

```
CG54007-05  MWGLLLALAAFAPAVGPALGAFRNSVLGLAQPGTTKVPGSTPALHSSPAQPPAETANGTS
CG54007_01  MWGLLLALAAFAPAVGPALGAFRNSVLGLAQPGTTKVPGSTPALHSSPAQPPAETANGTS
CG54007-04  MWGLLLALAAFAPAVGPALGAFRNSVLGLAQPGTTKVPGSTPALHSSPAQPPAETANGTS

CG54007-05  EQHVRIRVIKKKKVIMKKRKKLTLTRPTPLVTAGPLVTPTPAGTLDPAEKQETGCPPLGL
CG54007_01  EQHVRIRVIKKKKVIMKKRKKLTLTRPTPLVTAGPLVTPTPAGTLDPAEKQETGCPPLGL
CG54007-04  EQHVRIRVIKKKKVIMKKRKKLTLTRPTPLVTAGPLVTPTPAGTLDPAEKQETGCPPLGL

CG54007-05  ESLRVSDSRLEASSSQSFGLGPHRGRLNIQSGLEDGDLYDGAWCAEEQDADPWFQVDAGH
CG54007_01  ESLRVSDSRLEASSSQSFGLGPHRGRLNIQSGLEDGDLYDGAWCAEEQDADPWFQVDAGH
CG54007-04  ESLRVSDSRLEASSSQSFGLGPHRGRLNIQSGLEDGDLYDGAWCAEEQDADPWFQVDAGH

CG54007-05  PTRFSGVITQGRD-----PGLPSLRPQ---------------------------------
CG54007_01  PTRFSGVITQGRNSVWRYDWVTSYKVQFSNDSRTWWGSRNHSSGMDAVFPANSDPETPVL
CG54007-04  PTRFSGVITQGRNSVWRYDWVTSYKVQFSNDSRTWWGSRNHSSGMDAVFPANSDPETPVL

CG54007-05  ------------------------------------------------------------
CG54007_01  NLLPEPQVARFIRLLPQTWLQGGAPCLRAEILACPVSDPNDLFLEAPASGSSDPLDFQHH
CG54007-04  NLLPEPQVARFIRLLPQTWLQGGAPCLRAEILACPVSDPNDLFLEAPASGSSDPLDFQHH

CG54007-05  ------------------------------------------------------------
CG54007_01  NYKAMRKLMKQVQEQCPNITRIYSIGKSYQGLKLYVMEMSDKPGEHELGEPEVRYVAGMH
CG54007-04  NYKAMRKLMKQVQEQCPNITRIYSIGKSYQGLKLYVMEMSDKPGEHELGEPEVRYVAGMH

CG54007-05  ------------------------------------------------------------
CG54007_01  GNEALGRELLLLLMQFLCHEFLRGNPRVTRLLSEMRIHLLPSMNPDGYEIAYHRGSELVG
CG54007-04  GNEALGRELLLLLMQFLCHEFLRGNPRVTRLLSEMRIHLLPSMNPDGYEIAYHRGSELVG

CG54007-05  ------------------------------------------------------------
CG54007_01  WAEGRWNNQSIDLNHNFADLNTPLWEAQDDGKVPHIVPNHHLPLPTYYTLPNATVAPETR
CG54007-04  WAEGRWNNQSIDLNHNFADLNTPLWEAQDDGKVPHIVPNHHLPLPTYYTLPNATVAPETR

CG54007-05  ------------------------------------------------------------
CG54007_01  AVIKWMKRIPFVLSANLHGGELVVSYPFDMTRTPWAARELTPTPDDAVFRWLSTVYAGSN
CG54007-04  AVIKWMKRIPFVLSANLHGGELVVSYPFDMV------------------------------

CG54007-05  ------------------------------------------------------------
CG54007_01  LAMQDTSRRPCHSQDFSVHGNIINGADWHTVPGSMNDFSYLHTNCFEVTVELSCDKFPHE
CG54007-04  ------------------------------------------------------------

CG54007-05  ------------------------------------------------------------
CG54007_01  NELPQEWENNKDALLTYLEQVRMGIAGVVRDKDTELGIADAVIAVDGINHDVTTAWGGDY
CG54007-04  -----------------------------------------------TAS----------

CG54007-05  ------------------------------------------------------------
CG54007_01  WRLLTPGDYMVTASAEGYHSVTRNCRVTFEEGPFPCNFVLTKTPKQRLRELLAAGAKVPP
CG54007-04  --------------AEGYHSVTRNCRVTFEEGPFPCNFVLTKTPKQRLRELLAAGAKVPP

CG54007-05  ---------------
CG54007_01  DLRRRLERLRGQKD
CG54007-04  DLRRRLERLRGQKD
```
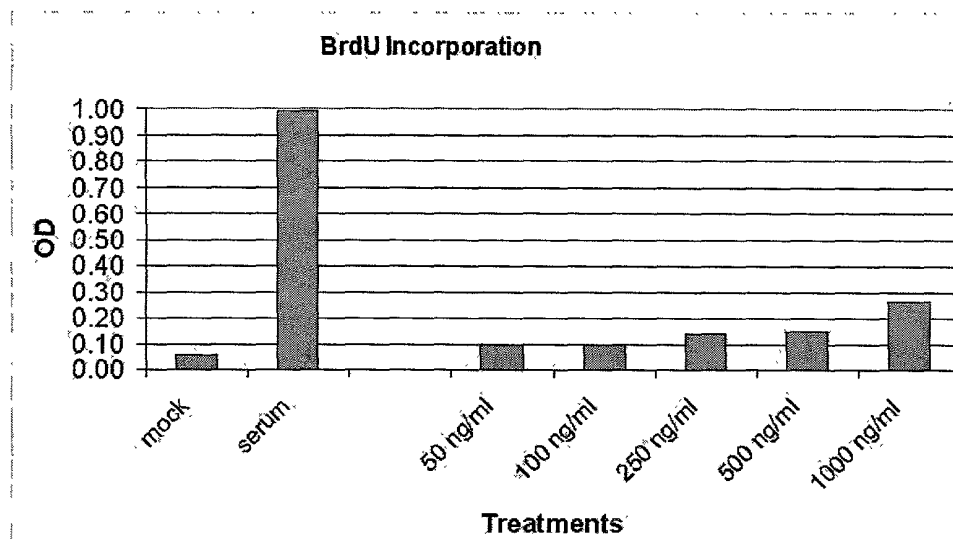
Fig.19

BrdU Incorporation

Fig. 20

Proliferation of NIH 3T3 Cells

Treatments: vehicle control, AL035460, 10 % serum

Y-axis: Cell Number (0, 50000, 100000, 150000, 200000, 250000, 300000, 350000, 400000)

X-axis: Treatments